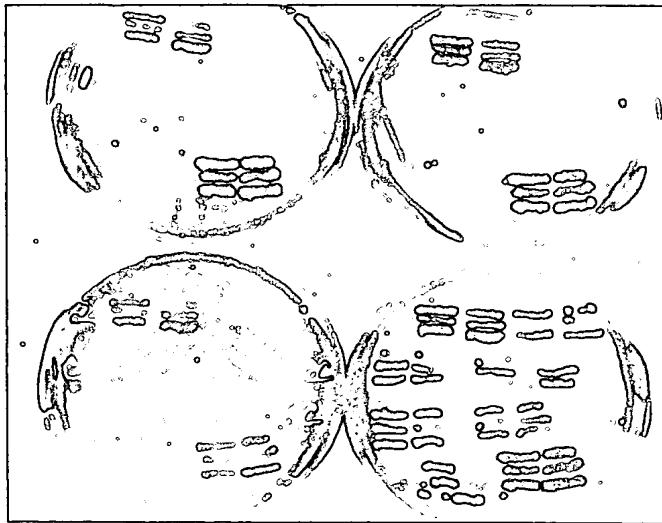


0 0 0 0 0 0 0 0 0 0 0 0



SC galactose, 100 mM KCl

SC glucose, 0mM KCl

SC galactose, 0 mM KCl

SC glucose, 100 mM KCl

FIG. 1

5' ...ACGGCATGCCGCGAGGTATATTCTTCTAGCTCAGTCAGCTTCGTTCCGGATTCTCTGGAGTGTATTCTTCAACAAATTGATCTAGTGCACATTCCGTCGAGC
 AACTACAAACACAGCGAAAGCCAAACGGCAATTAAGAAXXXXXXXATAATAAGCTAA
 -1

M1
 Met Ser Pro Asn Arg **Ile** Leu Ile Phe Tyr Ile Ser Tyr Leu Met Phe Gly Ala Ala Ile Tyr Tyr
 ATG TCG CCG AAT CGA ATC CTC CTG CTC ATC TTC TAC ATA TCC TAC CTG ATG TTC GGG GCG GCA ATC TAT TAC 75

H5-1
 His Ile Glu His Gly Glu Lys Ile Ser Arg Ala Glu Gln Arg Lys Ala Gln Ile Ala Ile Asn Glu Tyr Leu
 CAT ATT GAG CAC CGC GAG AAG ATA TCG CGC GAA CAG CGC AAG GCG CAA ATT GCA ATC AAC GAA TAT GCA TAT TAC 50
 G 60

Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Gln Asp Glu Ile Leu Gln Arg Ile Ser Asp Tyr Cys Asp Lys
 CTG GAG GAG CTC GGC GAC ACC ACA CAG GAT AGC ACC CCC TAC ACG TGG ACC TTC TAC CAT GCC TTC TTC GCC RTC 150

H5-1
 Pro Val Thr Leu Pro Pro Thr Tyr Asp Asp Thr Pro Tyr Thr Trp Thr Phe Tyr His Ala Phe Phe Ala Phe
 CCG GTT ACA TTG CCG ACA TAT GAT GAT ACC TAC AGC TGG ACC TTC TAC CAT GCC TTC TTC GCC RTC 300

M2
 Thr Val Cys Ser Thr Val Gly Tyr Gly Asn Ile Ser Pro Thr Thr Phe Ala Gly Arg Met Ile Met Ile Ala Tyr
 ACC GTT TGC TCC ACG GTG GGA TAT GGG AAT ATA TCG CCA ACC ACC TTC GCC GGA CGG ATG ATC ATG ATC GCG TAT 375

M3
 Ser Val Ile Gly Ile Pro Val Asn Gly Ile Leu Phe Ala Gly Leu Gly Glu Tyr Phe Gly Arg Thr Phe Glu Ala
 TCG GTG ATT GGC ATC CCC GTC AAT GGT ATC CTC TTT GCC GGC CTC GGC GAA TAC TTT GGA CGT ACG TTT GAA GCG 450

M4
 Ile Tyr Arg Tyr Lys Tyr Lys Met Ser Thr Asp Met His Tyr Val Pro Pro Gln Leu Gly Leu Ile Thr
 ATC TAC AGA CGC TCA AAA AAG ATG TCC ACC GAT ATG CAC TAT GTC CCG CAG CTG GGA TTG ATC ACC 525

M5-2
 Thr Val Val Ile Ala Leu Ile Pro Gly Ile Ala Leu Phe Leu Val Pro Cys Val Gly Val His Leu Leu Arg
 ACG GTG ATT GGC CTG ATT CCG CGA ATA GCT CTC TTC CTG GTG CCC TGC GTG GGT GTT CAC CTA CTT CGA 600

M6
 Glu Leu Gly Leu Ser Ile Ser Leu Tyr Ser Tyr Val Thr Thr Ile Gly Phe Gly Asp Tyr Val
 GAA CTG GGC CTA TCT TCC ATC TCG CTG TAC TAC ACC TAT GTG ACC ACC ACA ATT GGA TTC GGT GAC TAT GTG 675

M7
 Pro Thr Phe Gly Ala Asn Gln Pro Lys Glu Phe Gly Gly Trp Phe Val Val Tyr Gln Ile Phe Val Ile Val Trp
 CCC ACA TTT GGA GCC AAC CAG CCC AAG GAG TTC GGC TGG TTC GTG GTC TAT CAG ATC TTG ATC GTG TGG 750

M8
 Phe Ile Phe Ser Leu Gly Tyr Leu Val Met Ile Met Thr Phe Ile Thr Arg Gly Leu Gln Ser Lys Leu Ala
 TTC ATC TTC TCG CTC GGA TAT CTT GTG ATG ATC ATG ACA TTT ATC ACT CGG GGC CTC CAG AGC AAG AAG CTG GCA 825

M9
 Tyr Leu Glu Gln Leu Ser Ser Asn Leu Lys Ala Thr Gln Asn Arg Ile Trp Ser Gly Val Thr Lys Asp Val
 TAC CTG GAG CAG CTC TCC AAC CTC AAC GTC ACC AAT CGC ATC TGG TCT GGC GTC ACC AAG GAT GTG 900

M10
 Gly Tyr Leu Arg Arg Met Leu Asn Glu Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr Asp Val Asp Ile Ala
 GGC TAC CTC CGG CGA ATG CTC AAC GAG CTG TAC ATC CCT GTG ACC GAT GTA GAT ATC GCC 975

FIG. 2A

5' TTT GGT TGT CCG GAG

330 Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg
TAC ACA CTG CCA CGT TCC AAT TCG TGT CCG GAT CTG AGC ATG TAC CCC GTG GAG CCG GCT CCC ATT CCC AGC CGG 1050
360 Lys Arg Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly Met Val His Ala Asn Ser Asp
AAG AGG GCA TTC TCG GGC GAC ATG GTC GGC CAA AGG GAG GCG GGC ATG GTA CAC GCC AAT TCC GAT 1125
380 Thr Asp Leu Thr Lys Leu Asp Arg Glu Lys Thr Phe Glu Thr Ala Glu Ala TYR His Gln Thr Thr Asp Leu Leu
ACG GAT CTA ACC AAA CTG GAT CGC GAG AAG ACA TTC GAG ACC GCG TAC CAC CAG ACC GAT TTG CTG 1200
410 Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Ala Glu Gln Glu Asp Ala Ala Leu Tyr Gly GLY
GCC AAG GTG GTC AAC GCA CTG GCC ACG GTG AAG CCA CCG CCG GAA GAT GAA CAG GCA CCG GCG GCT TAT GGT GGC 1275
430 Tyr His Gly Phe Ser Asp Ser Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr Ser Pro
TAT CAT GGC TTC TCC GAC TCC CAG ATC CTC GCC AGC GAA TGG TCG TTC TCG ACG GTC AAC GAG TTC ACA TCA CCG 1350
460 Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg
CGA CGT CCA AGA CGT GCC TGC TCC GAT TTC AAT CTG GAG GCA CCT CGC TGG CAG AGC GAG CCA CTG CGT CGT 1425
480 Ser Ser His Asn Glu Trp Thr Trp Ser Gly Asp Asn Gln Gln Ile Gln Glu Ala Phe Asn Gln Arg Tyr Lys GLY
TCG AGC CAC AAC GAA TGG ACA TGG AGC GGC GAC AAC CAG CAG ATC CAG GAG GCA TTC AAC CAG CGC TAC AAG GGA 1500
510 Gln Gln Arg Ala Asn Gly Ala Ala Asn Ser Thr Met Val His Leu Glu Pro Asp Ala Leu Glu Gln Leu Arg
CAG CAG CGT GCC AAC GGA GCA GCC AAC TCG ACC ATG GTC CAT CTG GAG CCG GAT GCT TTG GAG CAG CAG CTG AGA 1575
530 Asn Asn His Arg Val Ala Ser Arg Ser Ser Pro Cys Arg Met Val Cys Asp Val Cys Phe Pro Ser Arg
AAC AAT CAC CGG GTG CGC GTC GCG TCA AGA AGT TCT CCA TGC CGG ATG GTC TGC GAC GTC TGT CCT TCC AGA 1650
560 Arg Ser Thr Pro Arg Arg Ile Trp Ser Ala Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg Arg Lys
AGA AGC ACC CCT CGC AGG ATC TGG AGC GCA AGT TGT CCG TGG TCT CGG TAC CCG AGG GTG TCA TCT CGC AGG AAG 1725
580 Pro Asp Pro Arg Trp Thr Thr Ser Thr Arg Ser Arg Arg Pro Pro Val Asn Pro Ile Cys Ala Thr Asp Ala
CCA GAT CCC CGC TGC ACT ACT ACA TCA ACA CGG TCA CGG CGG CCT CCA GTC AAT CCT ATT TGC GCA ACG GAC GCG 1800
610 Val Arg His Arg Pro Ser Asn Arg Met Ala Ala Trp Pro Ala Ala Ala Ala Gly TAA CGAACATGGCTTCAGATGGAG 1880
GATGGAGCAACCCGCCATCGGCCATTGGGGCATGGGAGCCATCAACGCCAAGGGGGCTGCTGGCAAGGCCGACGGAGCATCTCACCCAGAACATAA
GCCCATCGCTCGCCGGCGAGCATGTAATCGCCGACGGCTTGGCCAGATGGAGATGGACGGGGAGCTTGGCAACCAGTGGCTCTGGGA
TCGGCGGCCATGGGGCATGGGGAGCTGGGGCTGGGAGCATCGGCATCGGCTCTGACTATCGGCTCGTGGAGTCGATCTGATTCTGAGCTCGTGGAG . . .
TTCTCGGTTACCTCCGAAAAGGATATGAATGTTGCTGGAGCACGACCATTGCGGATCTGATTCGAGCTCGTGGCTCGTGGAG . . .

FIG. 2B

Met Ser Asp Gln Leu Phe Val Ala Phe Glu Lys Tyr Phe Leu Thr Ser Asn Glu Val Lys

ATG TCC GAT CAG CTG TTT GTC GCA TTT GAG AAG TAT TTC TTG ACG AGT AAC GAG GTC AAG
30 40 60

Lys Asn Ala Ala thr Glu Thr Trp Thr Phe Ser Ser Ser Ile Phe Phe Ala Val Thr Val
AAG AAT GCA GCA ACG GAG ACA TGG ACA ATT TCA TCG TCC ATT TTC TTT GCC GTA ACC GTC
M5-1 50 40

Val Thr Thr Ile Gly Tyr Gly Asn Pro Val Pro Val Thr Asn Ile Gly Arg Ile Pro Cys
GTC ACT ACC ATC GGA TAC GGT AAT CCA GTT CCA GTG ACA AAC ATT GGA CGG ATA TGG TGT
M2 70 60 120

Ile Ile Phe Ser Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Asp Leu Ala Gly
ATA TTG TTC TCC TTG CTT GGA ATA CCT CTA ACA CTG GTT ACC ATC GCT GAC TTG GCA GGT
90 80 180

Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys Leu Tyr Leu
AAA TTC CTA TCT GAA CAT CTT CGT TGG TTG TAT GGA AAC TAT TTG AAA TTA AAA TAT CTC
110 100 300

Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His Val Cys Glu His Ser His
ATA TTG TCA CGA CAT CGG AAA GAA CGG AGA GAG CAC GAG CAC TGT CAC AGT CAT
130 120 140

Gly Met Gly His Asp Met Asn Ile Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala
GGA ATG GGG CAT GAT ATG AAT ATC GAG GAG AAA AGA ATT CCT GCA TTC CTG GTA TTA GCT
M3 150 420 160

Ile Leu Ile Val Tyr Thr Ala Phe Gly Gly Val Ile Met Ser Lys Leu Glu Pro Trp Ser
ATT CTG ATA GTA TAT ACA GCG TTT GGC GGT GTC CTA ATG TCA AAA TTA GAG CCG TGG TCT
480 480

FIG. 3A

5' G T T G C T A T T C G C G

H5-2	
Phe	Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr
TTC	TTT ACT TCA TTC TAC TGG TCC TTC ATT ACA ATG ACT ACT GTC GGG TTT GGC GAC TGT
	190
Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu Tyr Ile Ile Leu Gly Lys Phe	
ATG CCC AGA AGG GAC GGA TAC ATG TAT ATC ATA TTG CTC TAT ATC ATT TTA GGT AAA TTT	
	210
Ser Met Lys Lys Gln Lys Phe Lys Ile Phe Leu Gly Leu Ala Ile Thr Met Cys	
TCA ATG AAA AAA CAA AAA TTC AAA ATA TTT TTA GGT CTT GCA ATA ACT ACA ATG TGC	
	230
Ile Asp Leu Val Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln	
ATT GAT TTG GTA GCA CTA CAG TAT ATT CGA AAG ATT CAT TAT TTC GGA AGA AAA ATT CAA	
	250
Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val Ser Glu Leu Tyr	
GAC GCT AGA TCT GCA TTG GCG GTT GTA GGA GGA AAG GTA GTC CTT GTA TCA GAA CTC TAC	
	270
Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser Arg Glu Ala Phe Ile Val Glu Asn	
GCA AAT TTA ATG CAA AAG CGA GCT CGT AAC ATG TCC CGA GAA GCT TTT ATA GTG GAG AAT	
	290
Leu Tyr Val Ser Lys His Ile Ile Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr	
CTC TAT GTT TCC AAA CAC ATC ATA CCA TTC ATA CCA ACT GAT ATC CGA TGT ATT CGA TAT	
	310
Ile Asp Gln Thr Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ala Ile Asp Met Gln	
ATT GAT CAA ACT GCC GAT GCT ACC ATT TCC ACG TCA TCG TCT GCA ATT GAT ATG CAA	
	330
Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys	
AGT TGT AGA TTT TGT CAT TCA AGA TAT TCT CTC AAT CGT GCA TTC AAA TAG	
	336
	1011

FIG. 3B

Ce orf1	MSPNRWILLL IFYISYLMFG AAIYYHIEHG EEKISRAEQR KAQIAINEYL	50
Dm orf1	50
Consensus	50
Ce orf1	--MSDQLFVA FEKYFLTSNE VKKNAATE[TW] TFSSSIFFFAV	38
Dm orf1	LEELGDKNTT TQDEILQRIS DYCDKPVTLP PTYDDTPY[TW] TFYHAFFFAF	100
Consensus[TW] TF.....FFA.	100
Ce orf1	[TVVTTTG]GYGN PVPVITNIGRI W[Q]ILFSLIGI PLTLVTIA[L] AGKFLSEHLV	88
Dm orf1	TVCST[V]GYGN ISPITTFAGRM IMIAYSVIGI PVNGILFACL	140
Consensus	TV...[T]GYGN ..P.T..GR. .I..S..GI P.....A.L.	150
Ce orf1	WLY[GNYLKLK YLILSRHRKE RREHVCE[H] SHGMGHDMMI EEKRIPAFLV	138
Dm orf1	--GEYFGRT FEAIYRRYKK YKMSTDMDHYV PPQLGLITTV VIALIPGIAL	187
Consensus	.G.Y.....R..K.H.G.IP....	200
Ce orf1	LAIILIVYTAF GGVLMSKLEP WSFFT[S]FYWS F[IT]MFTM[G]FG DLMPRRDGYM	188
Dm orf1	FLVLPCVGVH LLRELGLSS- -ISIYMS YVTTTT[G]FG DYVPT-FGAN	231
Consensus	.L..... .S.Y.S..[I]T[!]GFG D..P..G..	250
Ce orf1	YIILLYIILG KFSMKKKQKF KIFLGLAITT MCIDLVGMQY IRKIHYFGRK	238
Dm orf1	QPKEFGGWVF VYQIFVIVWF IFSLGYLVMI MTFITRGLOS KKLAYLEQQL	281
ConsensusF.....LG.....M.....G.Q.....	300
Ce orf1	IQDARSALAV VGGKVVLVSE LYANLMQKRA RNMSREAFIV ENLYVSKHII	288
Dm orf1	SSNLKATQNR IWSCVTKDVG YLRRMLNELY ILKVKPVYTD VDIAYTLPNS	331
ConsensusV.....	350
Ce orf1	PFI[P]DIRCI -RYIDQTADA AT[ST]SSSAI DMOSCRFCHS RYSLNRAFKX	337
Dm orf1	NSCPDLSMYR VEPAPIPSRK RAFSVCADMV G[A]REAGMVH ANSDTDLT[KL]	381
Consensus	.E.....S.....Q.....S.....S.....K.	400
Ce orf1	-----	337
Dm orf1	DREKTTFETAE AYHQTTDLLA KVVNALATVK PPPAEQEDAA LYGGYHGFSD	431
Consensus	450
Ce orf1	-----	337
Dm orf1	SQILASEWSF STVNEFTSPR RPRARACSDF NLEAPRWQSE RPLRSSHNEW	481
Consensus	500

FIG. 4

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mIRK
hROMK1
rGIRK1

Dm H5-1
Shak
Shal
Shab
Shaw
Eag
Slo

Dm H5-2

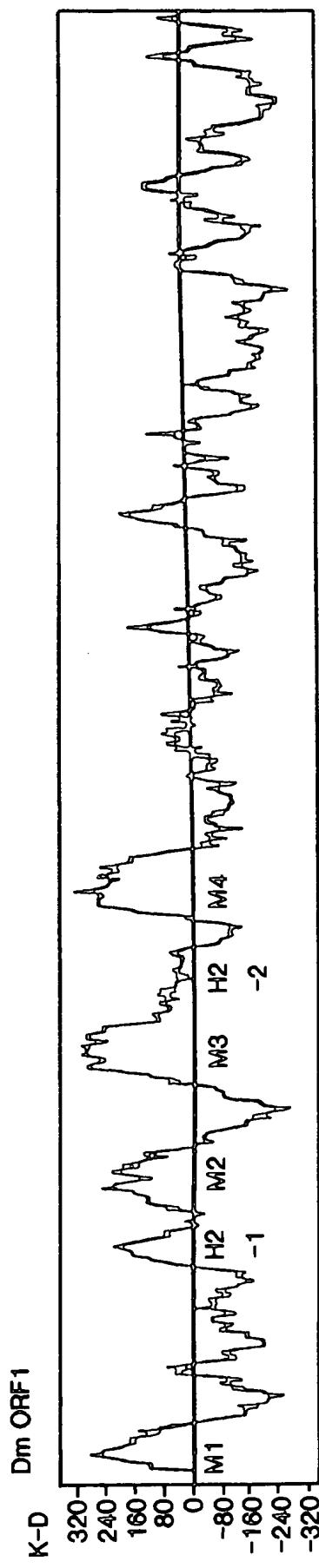
Dm H5-1
Ce 5-1
Dm H5-2
Ce H5-2

AFLFSIETQTTIGYGFRCTDECP
AFLFSLETQVTIGYGFRCTEQCA
AFLFFIETEATIGGYGYRYITDHCP
| | . | . | . | . | . | . |
AFFFAFTVCSTVGYGNISPTTFAG
| | . | . | . | . | . | . | . | . |
AFWWAVVTMTTVGYGDMTPVGFWG
AFWYTIVTMTTLGYGDMVPETIAG
AFWAGITMTTVGYGDI CPTTALG
GLWWALVTMTTVGYGDMAPKTYIG
ALYFTMTCMTSVGFGNVAAETDNE
CVYFLIVTMSTVGYGDVYCEVLG
. | | . | . | . | . | . | . | . |
SLYTSYVTTTIGFGDYVPTFGAN

{G,A,S,T}, {D,E}
{N,Q}, {K,R,H}
{F,Y,W} = {I,L,M,V}

FIG. 5A

0 0 0 0 0 0 0 0 0 0



K-D

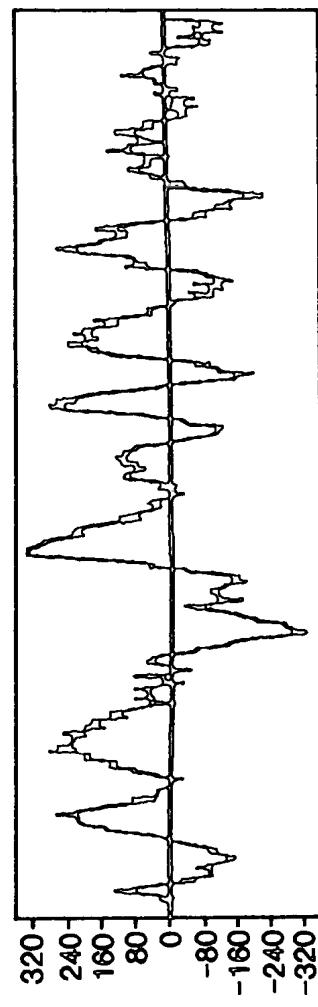
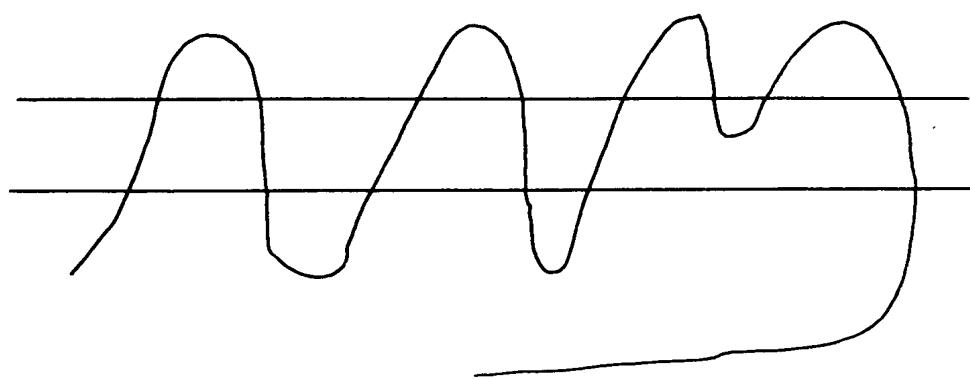


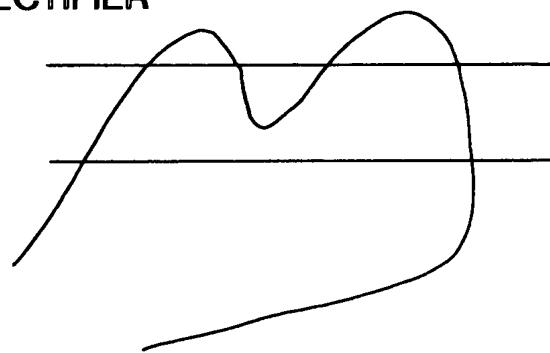
FIG. 5B

08016014 031107

1) SHAKER



2) INWARD RECTIFIER



3) ORF1

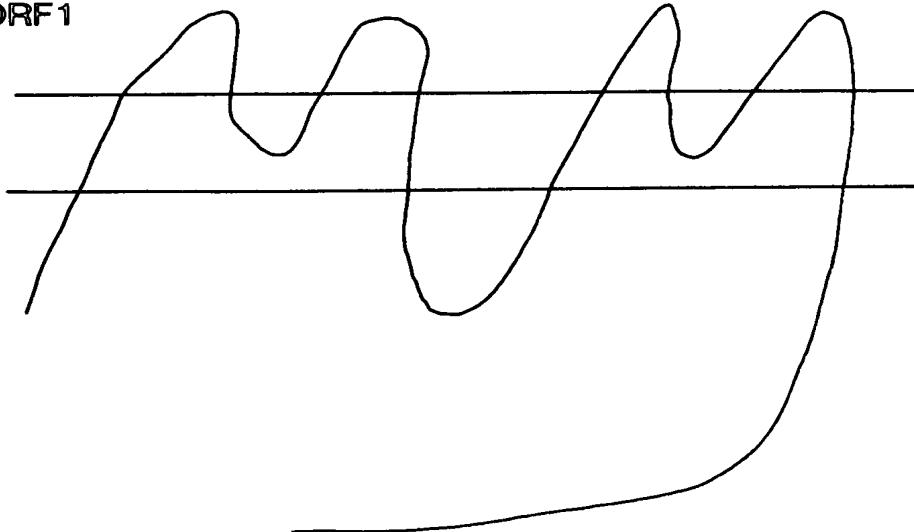


FIG. 6

08816044-031193

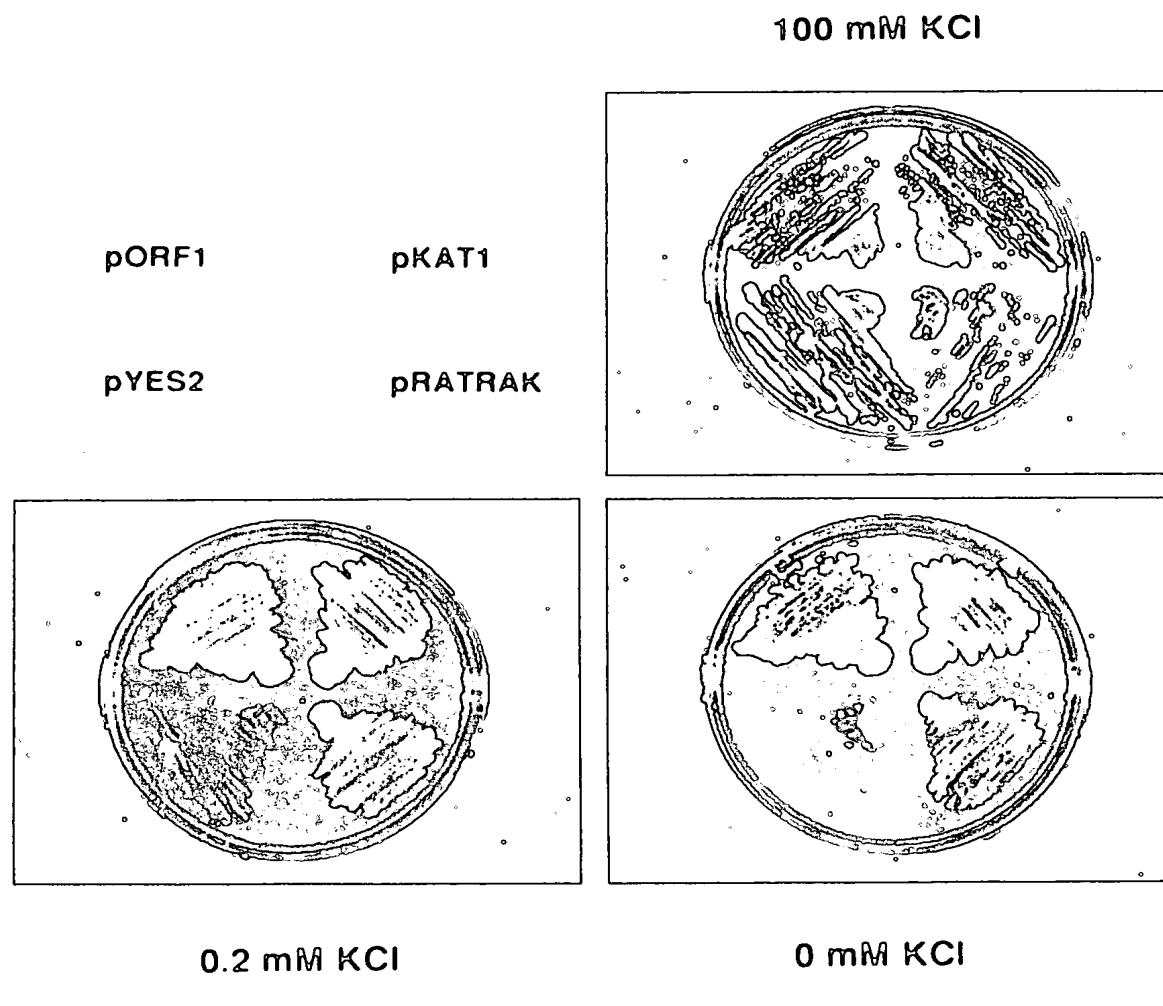
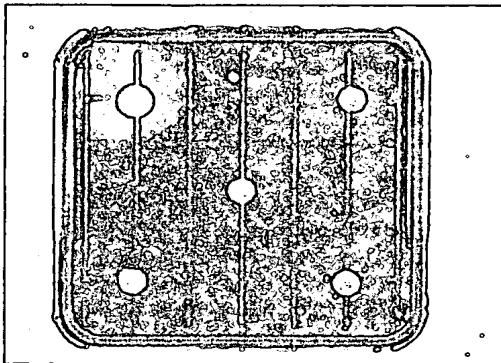


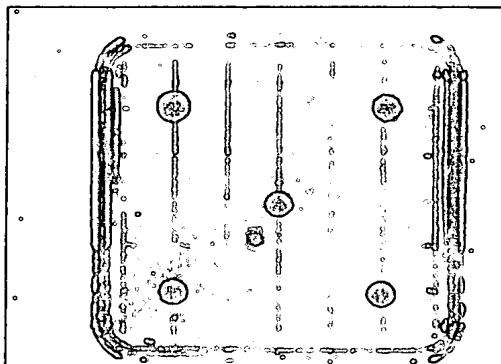
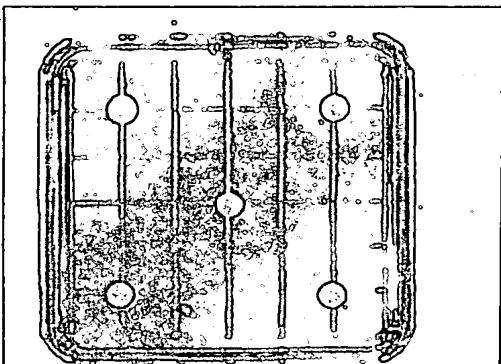
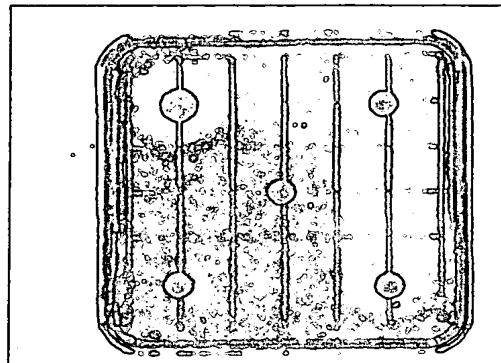
FIG. 7

088160412 031192

pORF1



pKAT1



pRATRAK

pYES2

FIG. 8

Met Val Ile Asn Arg Ser Asn Thr Tyr Ala Val Glu Gln Glu Ala Phe Pro Arg Asp Lys Tyr Asn Ile Val

ATG GTA ATA ATC AAC CGA TCG AAC ACC TAT GCC GTT GAG CAG GAA GCA TTT CCA AGA GAC AAG TAC AAT ATT GTC 75
30 Tyr Trp Leu Val Ile Leu Val **Gly Phe Gly Val Leu Leu Pro** Trp Asn Met Phe Ile Thr Ile Ala Pro Glu Tyr 50
TAC TGG CTC CTC ATT CTT GRT GGA TTC GGA GRT CTT CTG CCA TGG AAT ATG ATT ACT ATC GTC CCT GAG TAT 150

Tyr Val Asn Tyr Trp Phe Lys Pro Asp Gly Val Glu Thr Trp Tyr Ser Lys Glu Phe Met Gly Ser Leu Thr Ile 60
TAT GTG AAT TAT TGG TTC AAA CCG GAT GGC GTG GAG ACA TGG TAT TCG AAA GAA TTC ATG GGA TCT TTG ACG ATT 70
80 Gly Ser Gln Leu Pro Asn Ala Ser Ile Asn Val Phe Asn Leu Phe Leu Ile Ile Ala Gly Pro Leu Ile Tyr Arg
GGC TCA CAA CTT CCA AAC GCA AGC ATT AAT GTT TTC AAC CTC ATT GTC ATT GCT GGT CCC CTG ATC TAC CGC 300

100 Val Phe Ala Pro Val Cys Phe Asn Ile Val Asn Leu Thr Ile Ile Leu Ile Val Ile Val Glu Pro Thr
GTC TTT GCT CCG GTT TGC AAC ATC GTC AAC ATC GTC ATT CTC ATT CTC ATT GTC ATT GTC ATT GTC ATT GTC ATT CCC ACT 375
120 Glu Asp Ser Met Ser Trp Phe Trp Val Thr Leu Gly Met Ala Thr Ser Ile Asn Phe Ser Asn Gly Leu Tyr 140 150
GAA GAT TCC ATG TCC TGG TTT TFC TGG GTA ACT CTT GGA ATG GCG ACT TCA ATC AAT TTT AGC AAT GGG CTA TAT 450
160 Glu Asn Ser Val Tyr **Gly Val Gly Asp** Phe **Pro His Thr Tyr Ile Gly Ala Leu Ile Gly Asn Asn Ile**

GAA AAC TCG GTT TAT GGA GTT GGT GCG GAT TTT CCG CAC ACC TAC ATT GGC GCT CTC TTG ATT GGA AAC AAC ATT 525
180 Cys Gly Leu Leu Ile Thr Val Val Lys Ile Gly Val Thr Tyr Phe Leu Asn Asp Glu Pro Lys Leu Val Ala Ile
TGC GGA TTG CTG ATA ACG GTT GTG AAA ATC GGA GTG ACC TAT GAT GAG CCT AAA CTT GTC ATT GCA ATC 600
210 Val Tyr Phe Gly Ile Ser Leu Val Ile Leu Val Cys Ala Ile Ala Leu Phe Phe Ile Thr Lys Gln Asp Phe 220
GTC TAT TTC GGC ATA TCG TGT GTC ATC CTT CTT GCA ATT GCA TTT ACA AAG CAA GAT TTC 675

FIG. 9A

2' OH P₁ P₂ P₃ P₄ P₅ P₆

Tyr His His Gln Lys Glu Met Glu Ile Arg Glu Lys Ala Glu Thr Asp Arg Pro Ser Pro Ser Ile Leu	230	240	250
TAC CAC CAT CAA AAA GGA ATG GAA ACC GAC AGA GCG TCC TCA TCC ATT CTT CTT	750		
Trp Thr Thr Phe Thr Asn Cys Tyr Gly Gln Leu Phe Asn Val Trp Phe Cys Phe Ala Val Thr Leu Thr Ile Phe	260	270	
TGG ACC ACA TTC ACA AAC TGT TAT GGG CAA CTC CTC AAT TTC GAT TGG TGC TTT GCC GTC ACT CTC ACA ATC TTC	825		
Pro Val Met Met Thr Val Thr Thr Arg GLY Asp Ser GLY Phe Leu Asn Lys Ile Met Ser Glu Asn Asp Glu Ile	280	290	300
CCT GTR ATG ACC GTC ACT CGT GGA GAT TCC GGC TTC CTA AAC AAA ATT ATG TCT GAA AAC GAT GAA ATC	900		
Tyr Thr Leu Leu Thr Ser Phe Leu Val Phe Asn Leu Phe Ala Ala Ile GLY Ser Ile Val Ala Ser Lys Ile His	310	320	
TAC ACT TTG CTC ACA AGT TTC CTC GTC TTC AAT TTG TTC GCT GCG ATT GGA TCC ATA GTT GCT TCC ATT GAG ATT	975		
Trp Pro Thr Pro Arg Tyr Leu Lys Phe Ala Ile Ile Leu Arg Ala Leu Phe Ile Pro Phe Phe Phe Cys Asn	330	340	350
TGG CCG ACA CCC CGT TAC CTC AAA TTT GCC ATA ATC TTG CGT GCT GCT CTT TCC ATT CCA TTC ATT GCA TGC AAC	1050		
Tyr Arg Val Gln Thr Arg Ala Tyr Pro Val Phe Phe Glu Ser Thr Asp Ile Phe Val Ile GLY GLY Ile Ala Met	360	370	
TAT CGT GTC CAG ACG CGT CCT TAT CTC GCT TTT GAG TCT ACT GAC ATT TTT GTG ATT GGT GCA ATT GCC ATG	1125		
Ser Phe Ser His GLY Tyr Leu Ser Ala Leu Met GLY Tyr Thr Pro Asn Val Val Pro Ser His Tyr Ser Arg	380	390	400
TCT TTT TCA CAT GGA TAC CTC AGC GCT CTG GCA ATG GGA TAC ACT CCA AAC GTC GTG CCA TCT CAC TAC TCA AGA	1200		
Phe Ala Ala Gln Leu Ser Val Cys Thr Leu Met Val GLY Leu Leu Thr GLY GLY Leu Trp Pro Val Val Ile Glu	410	420	
TTT GCC GCT CAG CTT TCC GTC ACT CTC GAT GTC ATT GTC ACC GGT GGC CTC CCC GTC TGG CCC GTC ATT GAG	1275		
His Phe Val Asp LYS Pro Ser Ile Leu	430	434	
CAC TTC GTG GAC AAG CCA AGT ATC TTA TAA ATATTATAGCATTTAGAGTATACTGTTATATGTTAAGCTGTTTAAAGCTGTTGAAATAAA	1364		
ATAATTAAAAAA 1388			

FIG. 9B

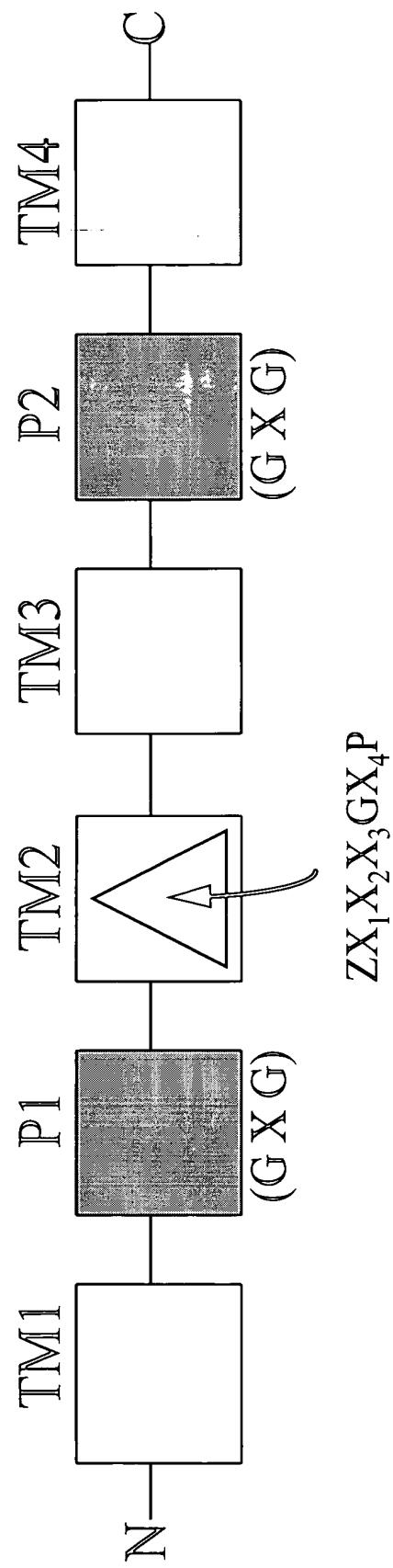


FIG. 10